

#16



S. Roark
RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/671,658A

DATE: 05/24/2002
TIME: 09:44:30

Input Set : N:\Crf3\RULE60\09671658A.RAW
Output Set: N:\CRF3\05242002\I671658A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gorman, Daniel M.
6 Mattson, Jeanine D.
8 (ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
9 Reagents

11 (iii) NUMBER OF SEQUENCES: 2

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: DNAX Research Institute
15 (B) STREET: 901 California Avenue
16 (C) CITY: Palo Alto
17 (D) STATE: California
18 (E) COUNTRY: USA
19 (F) ZIP: 94304-1104

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

ENTERED

27 (vi) CURRENT APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/09/671,658A
29 (B) FILING DATE: 27-Sep-2000
30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US/08/989,362
35 (B) FILING DATE: 12-DEC-1997
37 (A) APPLICATION NUMBER: US 60/032,846
38 (B) FILING DATE: 13-DEC-1996

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: Ching, Edwin P.
42 (B) REGISTRATION NUMBER: 34,090
43 (C) REFERENCE/DOCKET NUMBER: DX0686

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: (650)852-9196
47 (B) TELEFAX: (650)496-1204

50 (2) INFORMATION FOR SEQ. ID NO.: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 2191 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

61 (ix) FEATURE:

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62 (A) NAME/KEY: CDS
 63 (B) LOCATION: 125..1072
 66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 68 GCCAGGACCT CTGTGAACCG GTCGGGGCGG GGGCCGCCTG GCCGGGAGTC TGCTCGGCGG 60
 70 TGGGTGGCCG AGGAAGGGAG AGAACGATCG CGGAGCAGGG CGCCCGAACT CGGGCGCCG 120
 72 CGCC ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG TAC CTG CGC AGC TCG 169
 73 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser
 74 1 5 10 15
 76 GAG GAG ATG GGC AGC CCC GGC GTC CCA CAC GAG GGT CCG CTG CAC 217
 77 Glu Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His
 78 20 25 30
 80 CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA CCC GCC GCC TCC CGC 265
 81 Pro Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg
 82 35 40 45
 84 TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG GGC CAG GTG GTC TGC 313
 85 Ser Met Phe Leu Ala Leu Gly Leu Gly Leu Gly Gln Val Val Cys
 86 50 55 60
 88 AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG ATG GAT CCT AAC AGA 361
 89 Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg
 90 65 70 75
 92 ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA ATC CTG AGA CTC CAT 409
 93 Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His
 94 80 85 90 95
 96 GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG AGT GAA GAC ACA CTA 457
 97 Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu
 98 100 105 110
 100 CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT CAG GGG GCC GTG CAG 505
 101 Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln
 102 115 120 125
 104 AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC TTC TCA GGA GCT CCA 553
 105 Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro
 106 130 135 140
 108 GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC CAG CGA GGC AAG CCT 601
 109 Ala Met Met Glu Gly Ser Trp Leu Asp. Val Ala Gln Arg Gly Lys Pro
 110 145 150 155
 112 GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT GCT GCC AGC ATC CCA 649
 113 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 114 160 165 170 175
 116 TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG TAC CAC GAT CGA GGC 697
 117 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 118 180 185 190
 120 TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC GGA AAA CTA AGG GTT 745
 121 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 122 195 200 205
 124 AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC ATT TGC TTT CGG CAT 793
 125 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 126 210 215 220
 128 CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT CTT CAG CTG ATG GTG 841
 129 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val

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130	225	230	235														
132	TAT	GTC	GTT	AAA	ACC	AGC	ATC	AAA	ATC	CCA	AGT	TCT	CAT	AAC	CTG	ATG	889
133	Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
134	240				245				250				255				
136	AAA	GGA	GGG	AGC	ACG	AAA	AAC	TGG	TCG	GGC	AAT	TCT	GAA	TTC	CAC	TTT	937
137	Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
138						260				265			270				
140	TAT	TCC	ATA	AAT	GTT	GGG	GGA	TTT	TTC	AAG	CTC	CGA	GCT	GGT	GAA	GAA	985
141	Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
142						275				280			285				
144	ATT	AGC	ATT	CAG	GTG	TCC	AAC	CCT	TCC	CTG	CTG	GAT	CCG	GAT	CAA	GAT	1033
145	Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
146						290				295			300				
148	GCG	ACG	TAC	TTT	GGG	GCT	TTC	AAA	GTT	CAG	GAC	ATA	GAC	TGAGACTCAT		1082	
149	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
150						305				310			315				
152	TTCGTGGAAC	ATTAGCATGG	ATGTCCTAGA	TGTTGGAAA	CTTCTTAAAA	AATGGATGAT											1142
154	GTCTATACAT	GTGTAAGACT	ACTAAGAGAC	ATGGCCCACG	GTGTATGAAA	CTCACAGCCC											1202
156	TCTCTCTTGA	GCCTGTACAG	GTTGTGTATA	TGTAAAGTCC	ATAGGTGATG	TTAGATTATCAT											1262
158	GGTGATTACA	CAACGGTTT	ACAATTTGT	AATGATTTCC	TAAGAATTGA	ACCAAGATTGG											1322
160	GAGAGGTATT	CCGATGCTTA	TGAAAAAACTT	ACACGTGAGC	TATGGAAGGG	GGTCACAGTC											1382
162	TCTGGGTCTA	ACCCCTGGAC	ATGTGCCACT	GAGAACCTTG	AAATTAAGAA	GATGCCATGT											1442
164	CATTGCAAAG	AAATGATAGT	GTGAAGGGTT	AAAGTCTTTT	GAATTGTTAC	ATTGCGCTGG											1502
166	GACCTGCAA	TAAGTTCTTT	TTTCTTAATG	AGGAGAGAAA	AATATATGTA	TTTTTATATA											1562
168	ATGTCTAAAG	TTATATTCA	GGTGTATGT	TTTCTGTGCA	AAGTTTGTA	AATTATATTT											1622
170	GTGCTATAGT	ATTTGATTCA	AAATATTTAA	AAATGTCTCA	CTGTTGACAT	ATTTAATGTT											1682
172	TTAAATGTAC	AGATGTATT	AACTGGTGCA	CTTGTATT	CCCCTGAAGG	TACTCGTAGC											1742
174	TAAGGGGGCA	GAATACTGTT	TCTGGTGACC	ACATGTAGTT	TATTTCTTTA	TTCTTTTTAA											1802
176	CTTAATAGAG	TCTTCAGACT	TGTCAAAACT	ATGCAAGCAA	AATAAATAAA	AAAAAATAAA											1862
178	ATGAATATCT	TGAATAATAA	GTAGGATGTT	GGTCACCAGG	TGCCTTCAA	ATTTAGAAGC											1922
180	TAATTGACTT	TAGGAGCTGA	CATAGCCAA	AAGGATACAT	AATAGGCTAC	TGAAAATCTG											1982
182	TCAGGAGTAT	TTATGCAATT	ATTGAACAGG	TGTCTTTTT	TACAAGAGCT	ACAAATTGTA											2042
184	AATTTGTTT	CTTTTTTTC	CCATAGAAAA	TGTACTATAG	TTTATCAGCC	AAAAAAACAAT											2102
186	CCACTTTTA	ATTTAGTGAA	AGTTATTTA	TTATACTGTA	CAATAAAAGC	ATTGTTCTG											2162
188	AATGGCATT	TTTGGTACTT	AAAAATGGC														2191
191	(2) INFORMATION FOR SEQ ID NO: 2:																
193	(i) SEQUENCE CHARACTERISTICS:																
194	(A) LENGTH: 316 amino acids																
195	(B) TYPE: amino acid																
196	(D) TOPOLOGY: linear																
198	(ii) MOLECULE TYPE: protein																
200	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:																
202	Met	Arg	Arg	Ala	Ser	Arg	Asp	Tyr	Gly	Lys	Tyr	Leu	Arg	Ser	Ser	Glu	
203	1				5				10				15				
205	Glu	Met	Gly	Ser	Gly	Pro	Gly	Val	Pro	His	Glu	Gly	Pro	Leu	His	Pro	
206						20			25				30				
208	Ala	Pro	Ser	Ala	Pro	Ala	Pro	Ala	Pro	Pro	Pro	Ala	Ala	Ser	Arg	Ser	
209						35			40				45				
211	Met	Phe	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Leu	Gly	Gln	Val	Val	Cys	Ser	

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212	50	55	60
214	Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile		
215	65	70	75
			80
217	Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu		
218	85	90	95
220	Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro		
221	100	105	110
223	Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys		
224	115	120	125
226	Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala		
227	130	135	140
229	Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu		
230	145	150	155
			160
232	Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser		
233	165	170	175
235	Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp		
236	180	185	190
238	Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn		
239	195	200	205
241	Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His		
242	210	215	220
244	Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr		
245	225	230	235
			240
247	Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys		
248	245	250	255
250	Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr		
251	260	265	270
253	Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile		
254	275	280	285
256	Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala		
257	290	295	300
259	Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp		
260	305	310	315

VERIFICATION SUMMARY

PATENT APPLICATION: **US/09/671,658A**

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Input Set : N:\Crf3\RULE60\09671658A.RAW
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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]